beginning of the

their

simulation,

origins

scientists and

to

engineers embarked on another path: one in which is nature itself wh

spectacular

Genetic Algorithms Evolutionar

typical

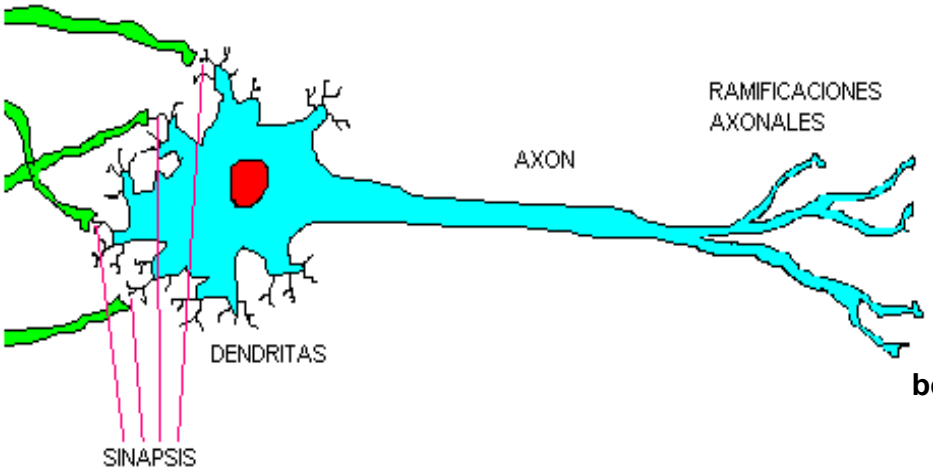
NEURAL NETWORKS (conn

human brain consists of millions of interconnected neurons.

learning models and approach inspired by th

neuron

collects signals from other neurons via structures called dendrites. Neuron delive



the

information

neurons These ramifications arrive until

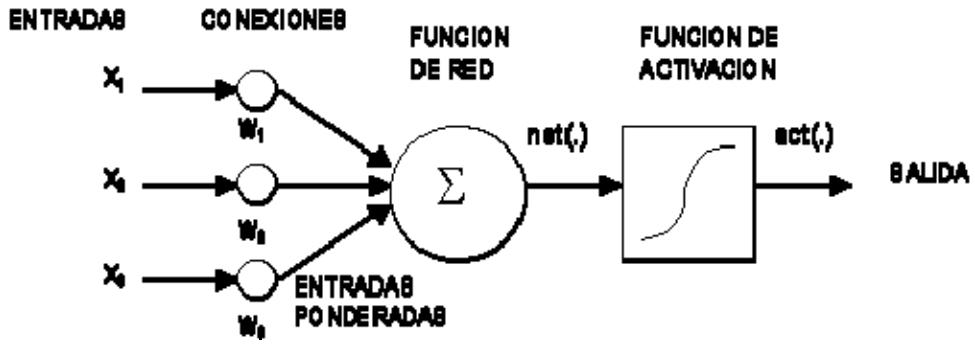
be dendrites

transmit

neurons and is being processed through synaptic connections and the neurons t

other from

some other


ENTRADAS
CONEXIONES
FUNCION
DE RED
FUNCION DE
ACTIVACION
net(.)
act(.)
SALIDA
ENTRADAS
PONDERADAS

Connections

function

a

synapse

the

or

Activation function Propagation Output Sign Weight Synaptic Artificial

	connection
	of the
	weight
	from
	one

ideas:

be

from located a active; or

Hebb set

concept

in

: the (synapses).

the

connections the from

connections be in

neurons

It represents

1949

neurons is strengthened if both are activated.

between between two

simultaneously

in fundamental

two neurons

Dartmouth IA. Here the first simul
publishes a

theory
of neural adaptation
and patterns inspired
by this theory,
Adaline (Adaptive
Linear Neuron) and
Madaline (Multiple Adaline). These models were used in numero

Perceptron, revealing serious limitations. This work created serious doub

critique of

of the

from

a serious

learning

perceptron

optical

1969)) made

identifier

results

Papert

delta,

be

1962)

they extended

to use continuous signals input and output.

published

allowed

binary

the

to

(Kohonen

trying

brain-state-in-a-box (BSB).

Sharon (Ellias,

1984) continues the work of Anderson and develops competitive

from

be based

Ritz

in

how

&

physiological

model

Jomnes

from

illustrative solves the problems posed by Minsky and Paper. In this decade, the reviva

East

group

on

highlights

the which

mechanisms algorithm

and retrieval of memory.

storage backpropagation,

remarkable

(Hinton

1986) and BAM models (Kos

are

& from

Sejnowski
is

decade

They

design a network must establish: Structure of ar

will be

units

sigmoidal activation radial

---

basis functions

organized in layers

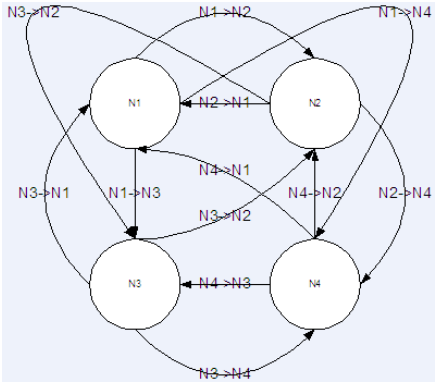
so that the output of a layer constitutes the input of th

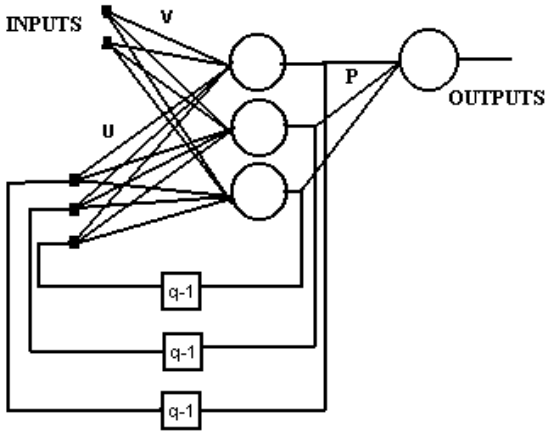
Hopfield

They have some type of feedback.

RNR ELMAN

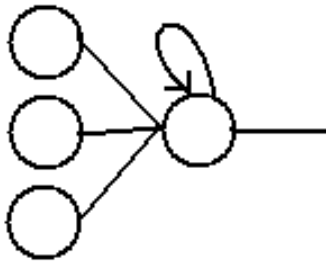
Hopfield, SOM, Elman RECURRING SECOND

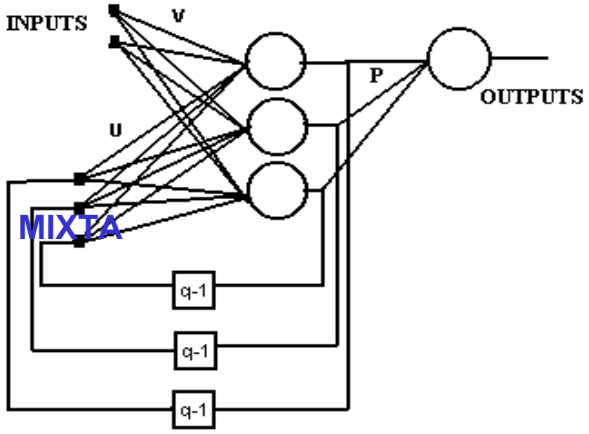


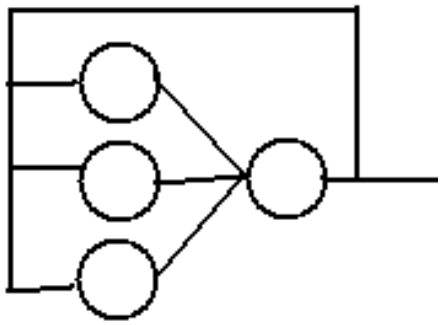


GLOBAL

Recurrence







Recurrence

the input-output

relationship of

the network captures the information in a table (X,

or

Be

approaches

interested

Since

models

cognitive

to

the previous one but

current

is

on

approach

of

all

the

taking

by

Connectionist

as its premise the biological plausibility of the models.

the

attempting

evolution

(which is not

such a theory, but a series of proven facts), was d

who

the theories,

inherited

discovered

that

necessary mechanism for evolution.

they providing they forgot and did not turn to rediscover until the

Mendel, who

that

were

the

isolation,

job

that

characters

the

the

in

Mendelian

total

They

of

deoxyribonucleic acid.

the
genes

is

about the same time, the

in

DNA,

John Holland at

algorithms.

later

the University of

be
genetic

become

Michigan in Ann

Arbor, "discover" genetic theory of natural selection

on

mechanisms

important

faced Holland genetic algorithms

of

the
natural

excessively

later, David Goldberg, current dolph

algorithms, Goldberg got what he wanted, writing a genetic algorithm on a pe

was an

genetic

complicated

apply

industrial engineer working on pipelines design, and

how

to

Applications
1985 ICGA'85. such a conference
the
accepted
same
held biannually.
they created
methods
for
celebrate the
by students
of
the
Biological
be
first
still
Holland

such that
genetic, (xi, ..., xn) is
be

about

..., xn)
from

a

find

(Xi,

encoding

on

and those from the crossing and returns to step evaluation.

new

population

selected

with

the

best

individuals who are selected for scoring, screening mechani

and mutation mechanism, termination condition.

coding to generate chromosomes, popul

Hybrid Algorithms.

for

have been developed for ea

we speak generically of Evolutionary Algorithms. Evolutionary program

give

place

to

the

called

change

of

discretely. The rule governing the transition of states in the ent

local transition rule.

*Automata, (*AC), it is a formal model com

cells, entities or *agents,*

a

elapses

instant

that time

assuming

to the

Next,

the ACs is its ability to provide

formed

to a set of rules common to all cells evolution.

may

defined

for

to be

equal for

particular instant of time.

in

set

all

a

only

finite

distributed in a n-dimensional regular

state

from

cells

cells PLC. The neighborhood influences the status change.

in

how

the

make

the

biological

the

cells

opposed

neighbors, so that an AC
a

be

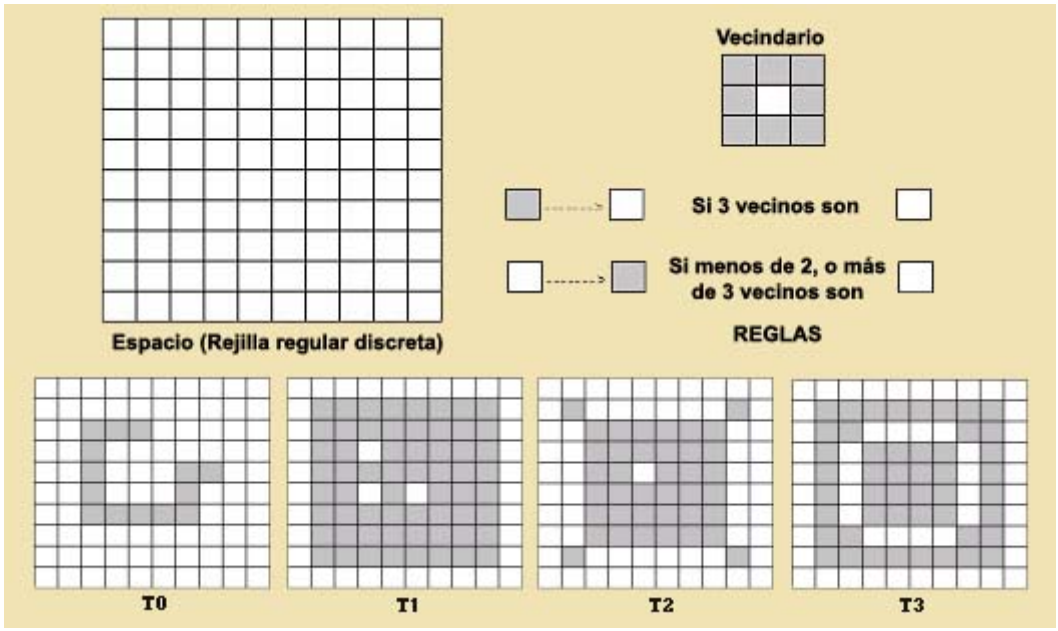
number of cells is finite, the
edges. The cells have no neighbors edges beyond the limits of the reticle.

considered

of the segment becomes a circle and a flat reticle s

of Life (**JV), devised by John Co**
where

example of the automaton defining the "Game of Li
the cells may be in a state of live (1) o



Cellular automaton "Game of Life".

Show that

from

Turing

machines

curious.

toward

the JV

from some initial configu

from

more states or

Universal

calculation

ls

equivalent

parallel

less

the

or

Cellular Automata

.

in

parallel.

Briefly,

exhaustive work of Stephen

Over the

Linear

quote

the

short

in

understand how

and return. since almost

the

search

a

its

livelihoods.

nest

substance

animals from

until

foods

the

pheromone, so that others can follow.

called

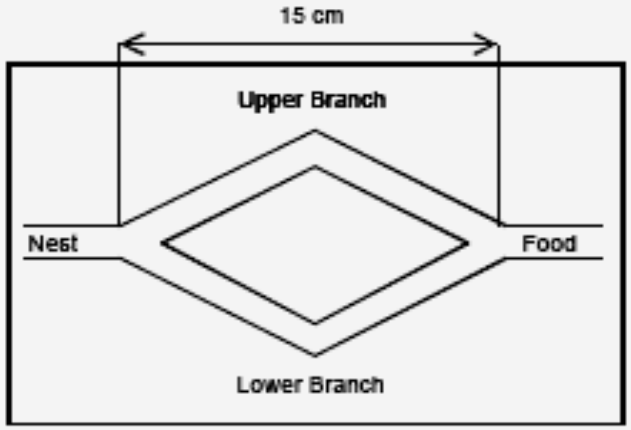
source

for

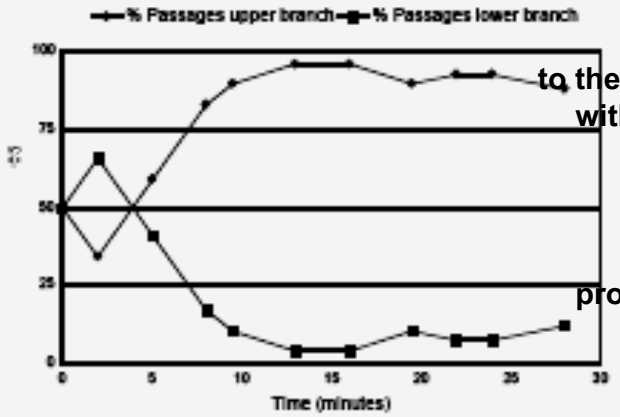
food their

following

decide



(a)



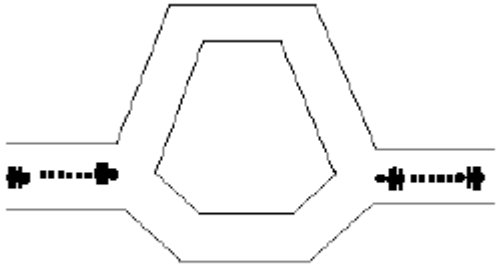
(b)

to the amount of pheromones proba

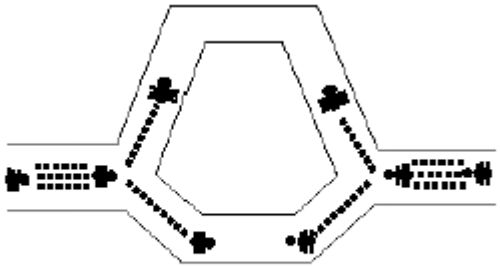
with

proportional

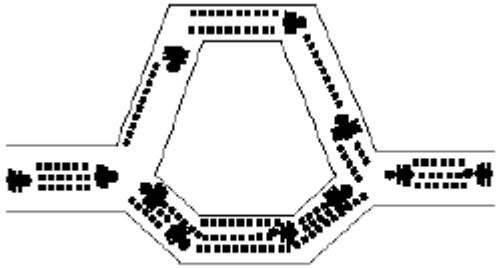
Figure 1. Single bridge experiment. (a) Experimental setup. (b) Results for a typical single trial, showing the percentage of passages on each of the two branches per unit of time as a function of time. Eventually, after an initial short transitory phase, the upper branch becomes the most used. After Deneubourg et al., 1990 [25].



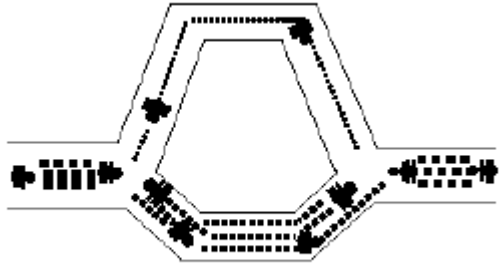
(a)



(b)



(c)



(d)

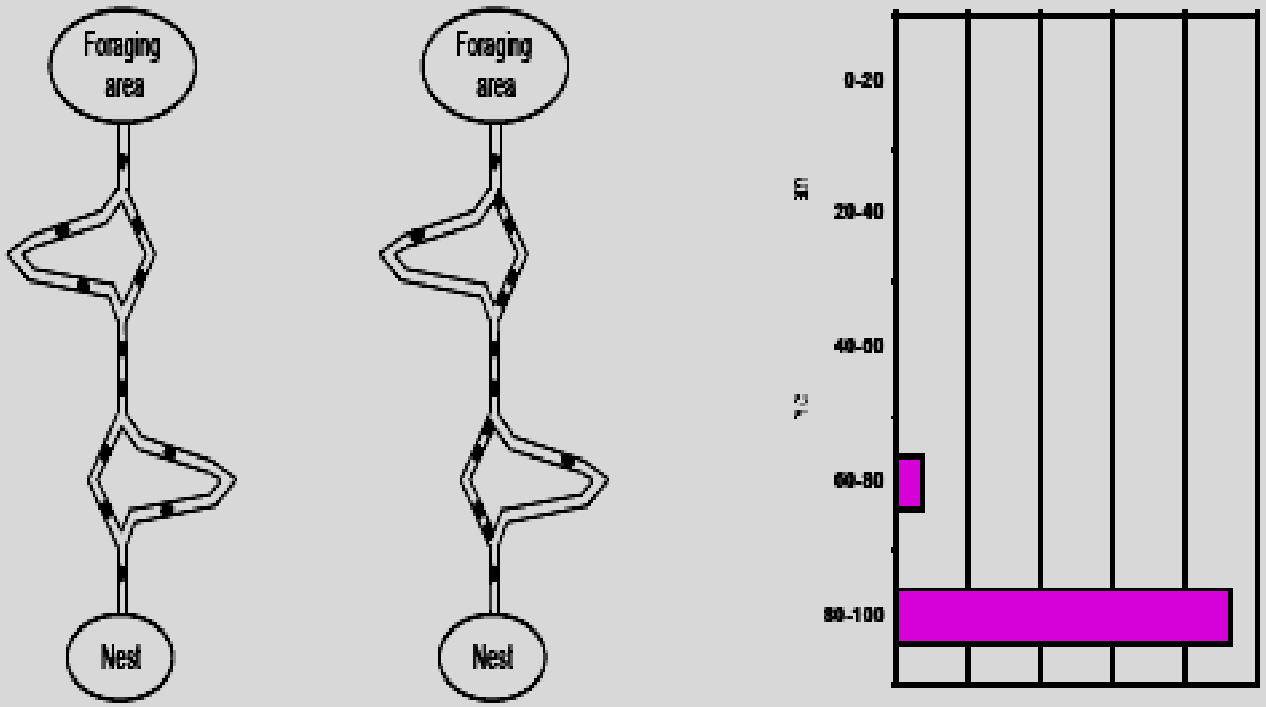


Figure 2. Double bridge experiment. (a) Ants start exploring the double bridge. (b) Eventually most of the ants choose the shortest path. (c) Distribution of the percentage of ants that selected the shorter path. After Goss et al. 1989 [60].

based on very simple agents ca

traveling salesman (Traveling Salesman Problem
TSP).
three

variants

algorithm

solving

all these methods are included within what is known as swarm intelligence.

for

Problem

theory

of

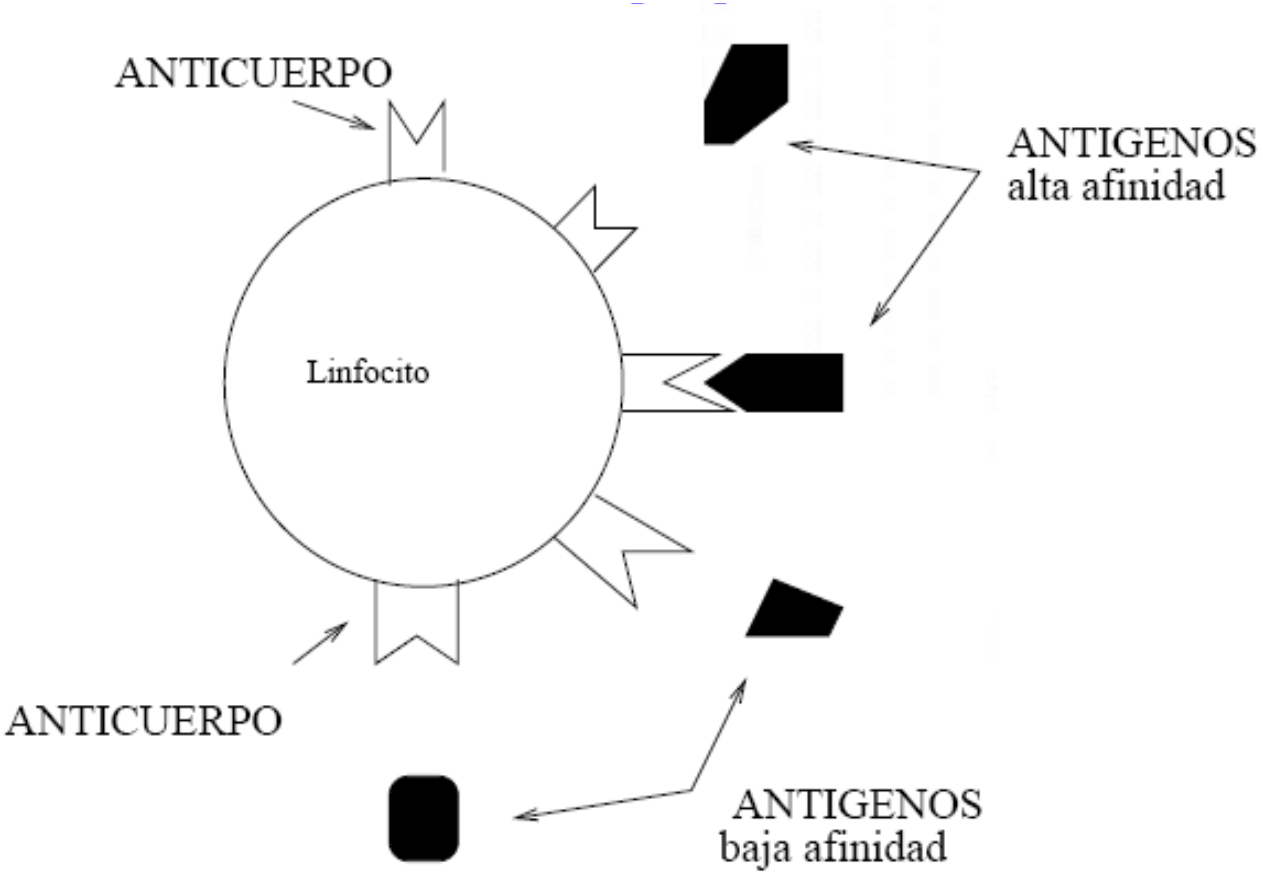
the
immunology

and patterns observed in the immune sys

principles

Y

functions,


ANTICUERPO
ANTIGENOS
alta afinidad
Linfocito
ANTICUERPO
ANTIGENOS
baja afinidad

Detection **system Decentralized Memory**

Diversity distributed autoregulatory

the essentials

from

mechanisms

immune system must possess.

for

evaluate

a

artificial

interactions,

because its scope is

very broad and very complex biologica

algorithm

are those based on the process o

emulate the process by which the immune system, in the presence of a spe

marrow models relate to the creation and maturatio

based on

the theory of immune network

the

the

Route

number of nodes.

first

Hamiltonian

Computing

where

computer-based DNA.

implementation

described

for

the

a

"Molecular

small

from

a

very

difficult to

computers because it is of type NP.

the

Conventional

central

vez.5. any

Hamiltonian Path problem

of

the solutions

solution

the graph has n nodes, retaining only those routes tha

routes

only those routes that start at the root node

using

remaining

appropriate biochemical equivalents of the steps for the specified algorithm.

DNA

set

was

are

DNA

taking those chains containing a certain pattern.

in

the
laboratories

and / or tempering, breaking or by ligating two DNA molecules with complementary s

computer DNA Model" Synthes

and

"non-restricted

called

limits

called ligase.. "Adherent"

mentioned

chains

PCR using a compound k

using from

they can

"program" one "DNA computer". DNA

a

used

with

compound

additional

to

70, the problem of the hour when the experiment successive possibility took about a week. for be the number can be used to encode the ' returns may, inducing from from molecule that too complex for a super-computer. Adleman still DNA a from nodes single It

whether

you want

run

You

need

about 1000 seconds to execute an instruction

Many

calculations

simultaneously

(parallel architecture), a computer as described can easily run 10 ^ 14 MIPS.

by the from current DNA Joule computers could from from storage Energy current run

means 10 ^ 10 times more efficient, Data can be stored in the D at run

an approximate density of 1 bit per cubic nanometer (nm ^{3}), require while x 10 10 the

recent

for example, the construction of pseudo-enzymes.
include,

automation, which no plus they can biological fast do. The that maybe possible be applications that require paralleli application electronic no East a very for